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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/069,082

DATE: 03/21/2003
 TIME: 13:45:24

Input Set : A:\P10890US.ST25.txt
 Output Set: N:\CRF4\03212003\J069082.raw

3 <110> APPLICANT: Quip Technology Limited
 5 <120> TITLE OF INVENTION: Retrovirus Assay
 7 <130> FILE REFERENCE: P10890US
 9 <140> CURRENT APPLICATION NUMBER: US 10/069,082
 C--> 10 <141> CURRENT FILING DATE: 2002-10-30
 12 <150> PRIOR APPLICATION NUMBER: GB 9919604.0
 13 <151> PRIOR FILING DATE: 1999-08-18
 15 <150> PRIOR APPLICATION NUMBER: PCT/GB00/03159
 16 <151> PRIOR FILING DATE: 2000-08-16
 18 <160> NUMBER OF SEQ ID NOS: 19
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 524
 24 <212> TYPE: PRT
 25 <213> ORGANISM: porcine endogenous retrovirus
 27 <400> SEQUENCE: 1
 29 Met Gly Gln Thr Val Thr Pro Leu Ser Leu Thr Leu Asp His Trp
 30 1 5 10 15
 33 Thr Glu Val Arg Ser Arg Ala His Asn Leu Ser Val Gln Val Lys Lys
 34 20 25 30
 37 Gly Pro Trp Gln Thr Phe Cys Ala Ser Glu Trp Pro Thr Phe Asp Val
 38 35 40 45
 41 Gly Trp Pro Ser Glu Gly Thr Phe Asn Ser Glu Ile Ile Leu Ala Val
 42 50 55 60
 45 Lys Ala Ile Ile Phe Gln Thr Gly Pro Gly Ser His Pro Asp Gln Glu
 46 65 70 75 80
 49 Pro Tyr Ile Leu Thr Trp Gln Asp Leu Ala Glu Asp Pro Pro Pro Trp
 50 85 90 95
 53 Val Lys Pro Trp Leu Asn Lys Pro Arg Lys Pro Gly Pro Arg Ile Leu
 54 100 105 110
 57 Ala Leu Gly Glu Lys Asn Lys His Ser Ala Glu Lys Val Glu Pro Ser
 58 115 120 125
 61 Ser Ser Tyr Leu Pro Arg Asp Arg Gly Ala Ala Asp Leu Ala Gly Thr
 62 130 135 140
 65 Pro Thr Cys Ser Pro Thr Pro Leu Ser Ser Thr Gly Cys Cys Glu Gly
 66 145 150 155 160
 69 Thr Ser Ala Pro Pro Gly Ala Pro Val Val Glu Gly Pro Ala Ala Gly
 70 165 170 175
 73 Thr Arg Ser Arg Arg Gly Ala Thr Pro Glu Arg Thr Asp Glu Ile Ala
 74 180 185 190
 77 Ile Leu Pro Leu Arg Thr Tyr Gly Pro Pro Met Pro Gly Gly Gln Leu
 78 195 200 205
 81 Gln Pro Leu Gln Tyr Trp Pro Phe Ser Ser Ala Asp Leu Tyr Asn Trp

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82 210 215 220
 85 Lys Thr Asn His Pro Pro Phe Ser Glu Asp Pro Gln Arg Leu Thr Gly
 86 225 230 235 240
 89 Leu Val Glu Ser Leu Met Phe Ser His Gln Pro Thr Trp Asp Asp Cys
 90 245 250 255
 93 Gln Gln Leu Leu Gln Thr Leu Phe Thr Thr Glu Glu Arg Arg Ile
 94 260 265 270
 97 Leu Leu Glu Ala Arg Lys Asn Val Pro Gly Ala Asp Gly Arg Pro Thr
 98 275 280 285
 101 Gln Leu Gln Asn Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly
 102 290 295 300
 105 Trp Asp Tyr Asn Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg
 106 305 310 315 320
 109 Gln Ala Leu Val Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn
 110 325 330 335
 113 Leu Ala Lys Val Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser
 114 340 345 350
 117 Val Phe Leu Glu Arg Leu Met Glu Ala Phe Arg Arg Phe Thr Pro Phe
 118 355 360 365
 121 Asp Pro Thr Ser Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile
 122 370 375 380
 125 Gly Gln Ser Ala Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly
 126 385 390 395 400
 129 Leu Gln Glu Ala Glu Leu Arg Asp Leu Val Arg Glu Ala Glu Lys Val
 130 405 410 415
 133 Tyr Tyr Arg Arg Glu Thr Glu Glu Lys Glu Gln Arg Lys Glu Lys
 134 420 425 430
 137 Glu Arg Glu Glu Arg Glu Glu Arg Arg Asp Arg Arg Gln Glu Lys Asn
 138 435 440 445
 141 Leu Thr Lys Ile Leu Ala Ala Val Val Glu Gly Lys Ser Ser Arg Glu
 142 450 455 460
 145 Arg Glu Arg Asp Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly
 146 465 470 475 480
 149 Asn Leu Gly Asn Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys
 150 485 490 495
 153 Lys Glu Lys Gly His Trp Ala Arg Asn Cys Pro Lys Lys Gly Asn Lys
 154 500 505 510
 157 Gly Pro Lys Val Leu Ala Leu Glu Glu Asp Lys Asp
 158 515 520
 161 <210> SEQ ID NO: 2
 162 <211> LENGTH: 660
 163 <212> TYPE: PRT
 164 <213> ORGANISM: porcine endogenous retrovirus Type PERV A
 166 <400> SEQUENCE: 2
 168 Met His Pro Thr Leu Ser Arg Arg His Leu Pro Ile Arg Gly Gly Lys
 169 1 5 10 15
 172 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
 173 20 25 30
 176 Leu Thr Leu Ser Ile Thr Pro Gln Val Asn Gly Lys Arg Leu Val Asp

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177	35	40	45
180	Ser Pro Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Leu Thr Asp		
181	50	55	60
184	Ser Gly Thr Gly Ile Asn Ile Asn Ser Thr Gln Gly Glu Ala Pro Leu		
185	65	70	75
188	Gly Thr Trp Trp Pro Glu Leu Tyr Val Cys Leu Arg Ser Val Ile Pro		80
189	85	90	95
192	Gly Leu Asn Asp Gln Ala Thr Pro Pro Asp Val Leu Arg Ala Tyr Gly		
193	100	105	110
196	Phe Tyr Val Cys Pro Gly Pro Pro Asn Asn Glu Glu Tyr Cys Gly Asn		
197	115	120	125
200	Pro Gln Asp Phe Phe Cys Lys Gln Trp Ser Cys Ile Thr Ser Asn Asp		
201	130	135	140
204	Gly Asn Trp Lys Trp Pro Val Ser Gln Gln Asp Arg Val Ser Tyr Ser		
205	145	150	155
208	Phe Val Asn Asn Pro Thr Ser Tyr Asn Gln Phe Asn Tyr Gly His Gly		
209	165	170	175
212	Arg Trp Lys Asp Trp Gln Gln Arg Val Gln Lys Asp Val Arg Asn Lys		
213	180	185	190
216	Gln Ile Ser Cys His Ser Leu Asp Leu Asp Tyr Leu Lys Ile Ser Phe		
217	195	200	205
220	Thr Glu Lys Gly Lys Gln Glu Asn Ile Gln Lys Trp Val Asn Gly Ile		
221	210	215	220
224	Ser Trp Gly Ile Val Tyr Tyr Gly Gly Ser Gly Arg Lys Lys Gly Ser		
225	225	230	235
228	240	245	250
229	Val Leu Thr Ile Arg Leu Arg Ile Glu Thr Gln Met Glu Pro Pro Val		
232	255	260	265
233	270	275	280
236	270	275	285
237	285	290	295
240	295	300	305
244	305	310	315
245	320	325	330
248	325	330	335
249	335	340	345
252	350	355	360
253	360	365	370
256	365	370	375
257	380	385	390
260	385	390	395
261	400	405	410
264	405	410	415
268	415	420	425
269	425	430	
272			
273			

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276 Val Met Val Gln Ile Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala
277 435 440 445
280 Val Leu Asp Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro
281 450 455 460
284 Ile Ser Leu Thr Leu Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly
285 465 470 475 480
288 Val Gly Thr Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu
289 485 490 495
292 Lys Gly Leu Ser Asn Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala
293 500 505 510
296 Leu Glu Lys Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser
297 515 520 525
300 Glu Val Val Leu Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys
301 530 535 540
304 Glu Gly Gly Leu Cys Val Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val
305 545 550 555 560
308 Asp His Ser Gly Ala Ile Arg Asp Ser Met Ser Lys Leu Arg Glu Arg
309 565 570 575
312 Leu Glu Arg Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu
313 580 585 590
316 Gly Trp Phe Asn Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu
317 595 600 605
320 Thr Gly Pro Leu Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys
321 610 615 620
324 Leu Ile Asn Arg Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val
325 625 630 635 640
328 Gln Ile Met Val Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly
329 645 650 655
332 Glu Thr Asp Leu
333 660
336 <210> SEQ ID NO: 3
337 <211> LENGTH: 638
338 <212> TYPE: PRT
339 <213> ORGANISM: porcine endogenous retrovirus Type PERV MSL
341 <400> SEQUENCE: 3
343 Met His Pro Thr Leu Asn Arg Arg His Leu Pro Ile Arg Gly Gly Lys
344 1 5 10 15
347 Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
348 20 25 30
351 Leu Thr Leu Ser Ile Thr Ser Gln Thr Asn Gly Met Arg Ile Gly Asp
352 35 40 45
355 Ser Leu Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Ile Thr Asp
356 50 55 60
359 Ser Gly Thr Gly Ile Asn Ile Asn Asn Thr Gln Gly Glu Ala Pro Leu
360 65 70 75 80
363 Gly Thr Trp Trp Pro Asp Leu Tyr Val Cys Leu Arg Ser Val Ile Pro
364 85 90 95
367 Ser Leu Thr Ser Pro Pro Asp Ile Leu His Ala His Gly Phe Tyr Val
368 100 105 110

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371 Cys Pro Gly Pro Pro Asn Asn Gly Lys His Cys Gly Asn Pro Arg Asp
372 115 120 125
375 Phe Phe Cys Lys Gln Trp Asn Cys Val Thr Ser Asn Asp Gly Tyr Trp
376 130 135 140
379 Lys Trp Pro Thr Ser Gln Gln Asp Arg Val Ser Phe Ser Tyr Val Asn
380 145 150 155 160
383 Thr Tyr Thr Ser Ser Gly Gln Phe Asn Tyr Leu Thr Trp Ile Arg Thr
384 165 170 175
387 Gly Ser Pro Lys Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser
388 180 185 190
391 Phe Thr Glu Lys Gly Lys Gln Glu Asn Ile Leu Lys Trp Val Asn Gly
392 195 200 205
395 Met Ser Trp Gly Met Val Tyr Tyr Gly Ser Gly Lys Gln Pro Gly
396 210 215 220
399 Ser Ile Leu Thr Ile Arg Leu Lys Ile Asn Gln Leu Glu Pro Pro Met
400 225 230 235 240
403 Ala Ile Gly Pro Asn Thr Val Leu Thr Gly Gln Arg Pro Pro Thr Gln
404 245 250 255
407 Gly Pro Gly Pro Ser Ser Asn Ile Thr Ser Gly Ser Asp Pro Thr Glu
408 260 265 270
411 Ser Asn Ser Thr Thr Lys Met Gly Ala Lys Leu Phe Ser Leu Ile Gln
412 275 280 285
415 Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro Glu Ala Thr Ser Ser
416 290 295 300
419 Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr Tyr Glu Gly Met Ala
420 305 310 315 320
423 Arg Arg Gly Lys Phe Asn Val Thr Lys Glu His Arg Asp Gln Cys Thr
424 325 330 335
427 Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu Val Ser Gly Lys Gly
428 340 345 350
431 Thr Cys Ile Gly Lys Val Pro Pro Ser His Gln His Leu Cys Asn His
432 355 360 365
435 Thr Glu Ala Phe Asn Gln Thr Ser Glu Ser Gln Tyr Leu Val Pro Gly
436 370 375 380
439 Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Val Ser
440 385 390 395 400
443 Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys Ile Met Val Gln Ile
444 405 410 415
447 Val Pro Arg Val Tyr Tyr Pro Glu Lys Ala Ile Leu Asp Glu Tyr
448 420 425 430
451 Asp Tyr Arg Asn His Arg Gln Lys Arg Glu Pro Ile Ser Leu Thr Leu
452 435 440 445
455 Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly Val Gly Thr Gly Thr
456 450 455 460
459 Ala Ala Leu Val Thr Gly Pro Gln Gln Leu Glu Thr Gly Leu Ser Asn
460 465 470 475 480
463 Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala Leu Glu Lys Ser Val
464 485 490 495
467 Ser Asn Leu Glu Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln

VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date